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Abstract

Mycobacterium marinum (Mm) is one of the closest genetic relative to *Mycobacterium tuberculosis* (Mtb), the bacterium that causes human TB, it establishes chronic infections in a variety of fish species and presents similar pathology. We extend the recently developed model of Mm transmission dynamics in aquatic animals, by allowing the intra-host progression rates to be sampled from an unknown probability distribution. This more general model consists of a nonlinear hyperbolic partial differential equation coupled with five nonlinear ordinary differential equations. We develop a second order approximation scheme to approximate the solution, and establish the convergence to a unique bounded variation weak solution of the model. We also provide examples of the approximated model and improved agreement to data.